

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:09:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819078.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1819078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:09:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	712,187
Mapped reads	649,632 / 91.22%
Unmapped reads	62,555 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,395 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	14,422 / 2.03%
Duplication rate	1.65%
Clipped reads	650,090 / 91.28%

2.2. ACGT Content

Number/percentage of A's	9,650,112 / 25.6%
Number/percentage of C's	7,051,960 / 18.7%
Number/percentage of T's	11,486,765 / 30.47%
Number/percentage of G's	9,513,457 / 25.23%
Number/percentage of N's	612 / 0%
GC Percentage	43.94%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.1378
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2.4. Mapping Quality

Mean Mapping Quality	44.52
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2.5. Mismatches and indels

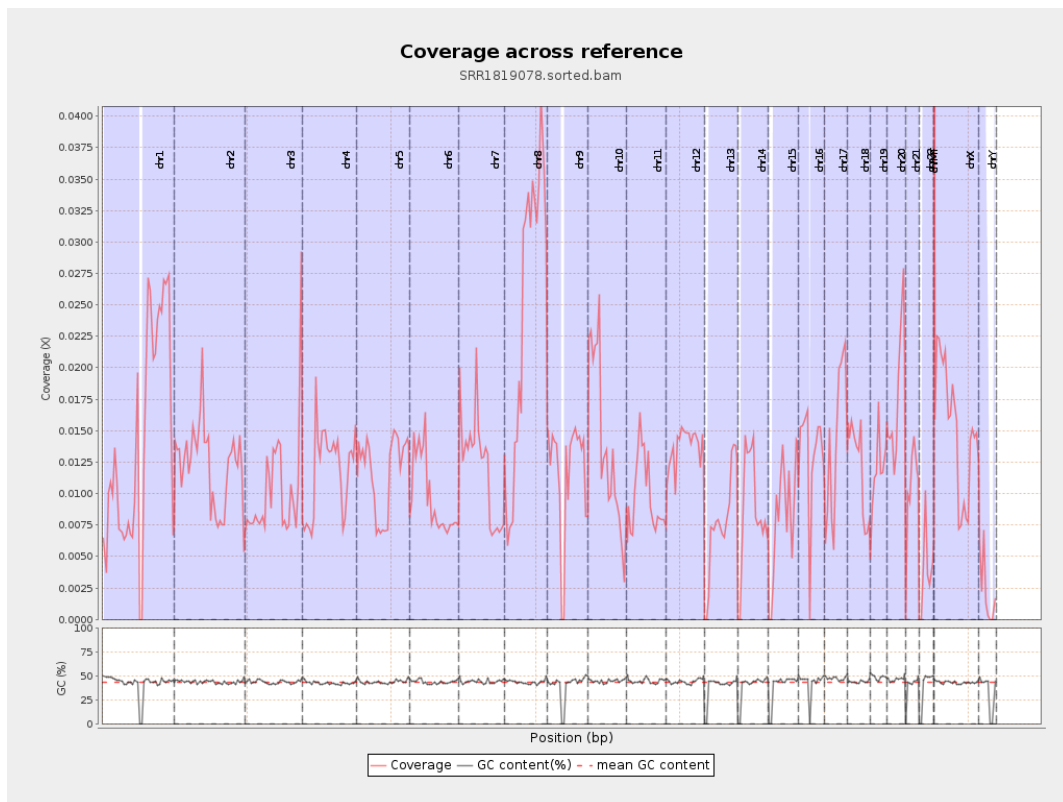
General error rate	0.53%
Mismatches	192,965
Insertions	2,616
Mapped reads with at least one insertion	0.4%
Deletions	6,852
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.97%

2.6. Chromosome stats

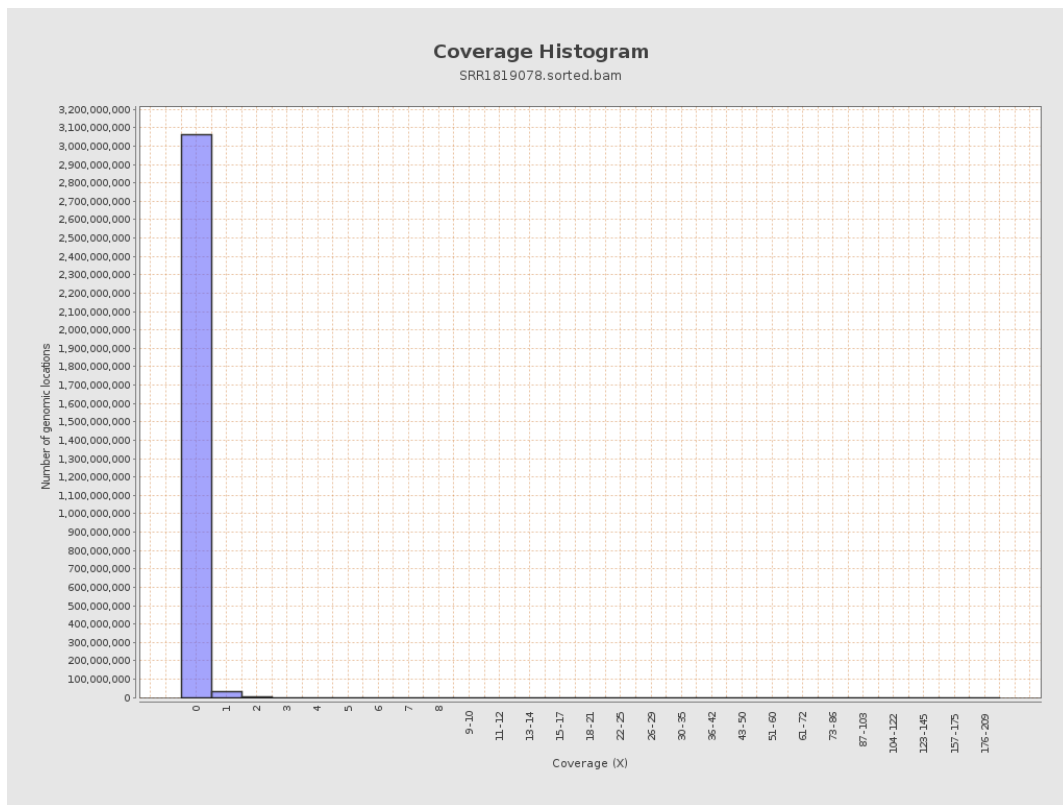
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3472992	0.0139	0.1873
chr2	243199373	2991145	0.0123	0.1567
chr3	198022430	2000842	0.0101	0.1055
chr4	191154276	2250714	0.0118	0.1213
chr5	180915260	2125338	0.0117	0.1132
chr6	171115067	1660231	0.0097	0.1104
chr7	159138663	1937582	0.0122	0.1671

chr8	146364022	3567924	0.0244	0.1772
chr9	141213431	1660302	0.0118	0.1273
chr10	135534747	1890597	0.0139	0.1552
chr11	135006516	1338489	0.0099	0.1365
chr12	133851895	1832633	0.0137	0.1227
chr13	115169878	883063	0.0077	0.0905
chr14	107349540	936464	0.0087	0.0993
chr15	102531392	849383	0.0083	0.0968
chr16	90354753	1178083	0.013	0.1248
chr17	81195210	1137450	0.014	0.129
chr18	78077248	941131	0.0121	0.2021
chr19	59128983	712471	0.012	0.1524
chr20	63025520	1125483	0.0179	0.1398
chr21	48129895	509711	0.0106	0.1125
chr22	51304566	208878	0.0041	0.0667
chrMT	16571	5873	0.3544	0.6527
chrX	155270560	2367090	0.0152	0.1356
chrY	59373566	130375	0.0022	0.0708

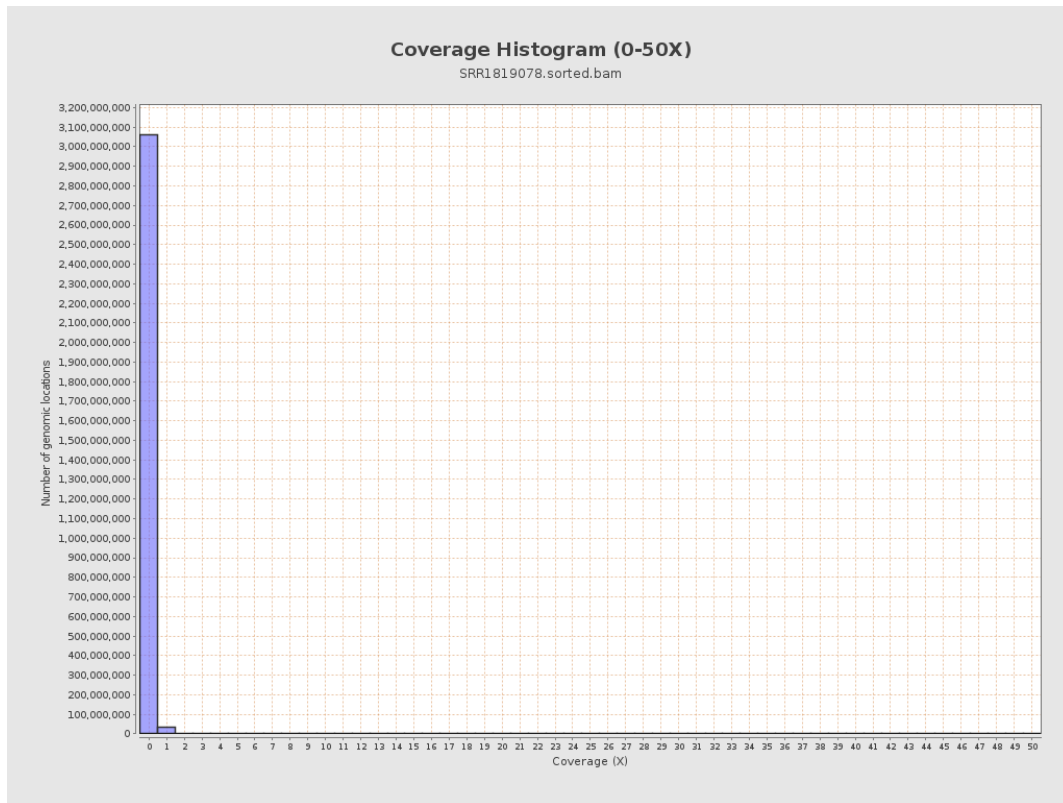
3. Results : Coverage across reference



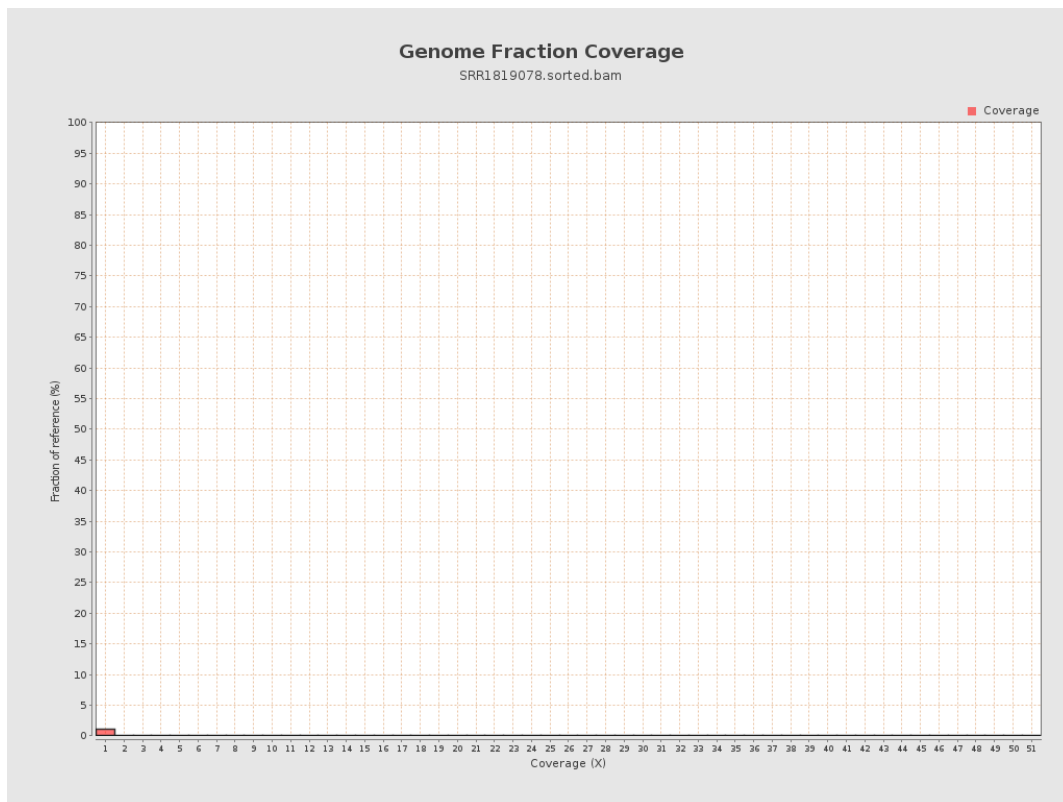
4. Results : Coverage Histogram



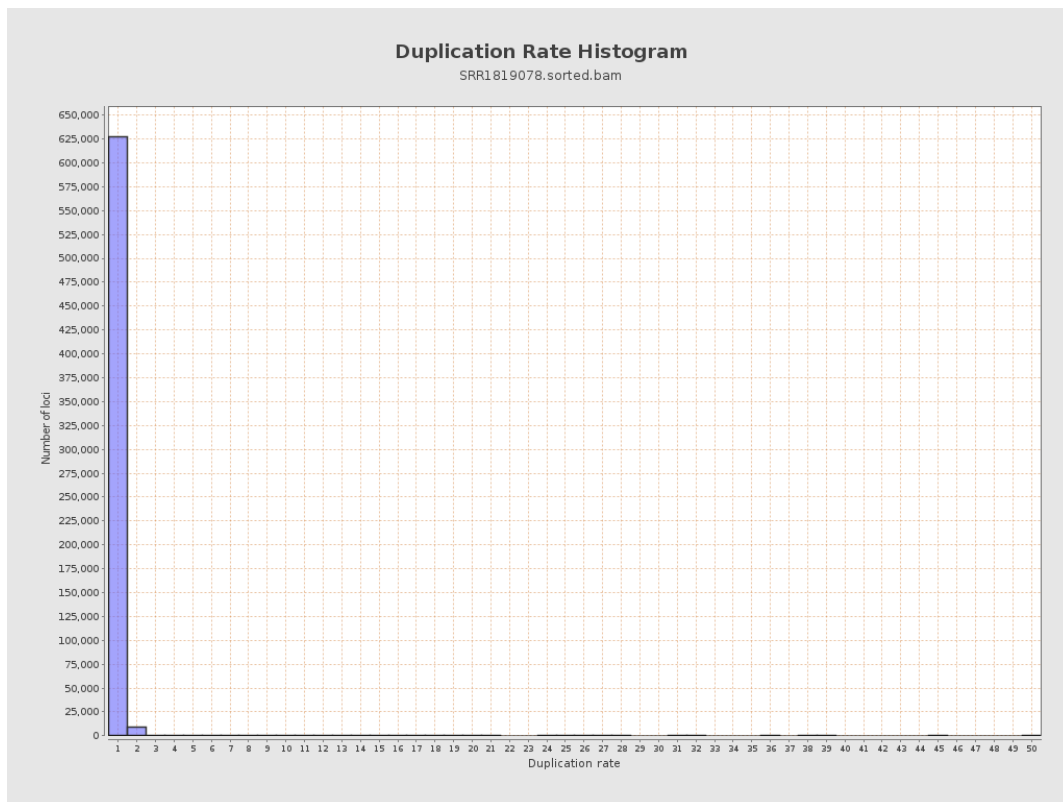
5. Results : Coverage Histogram (0-50X)



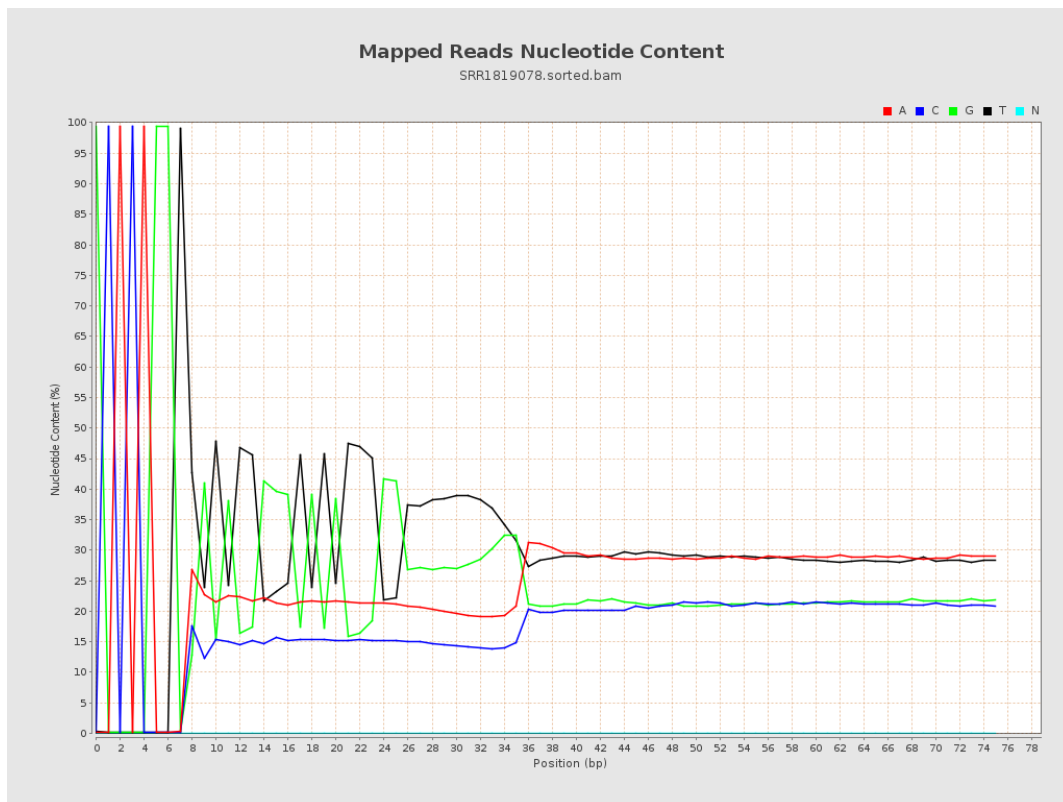
6. Results : Genome Fraction Coverage



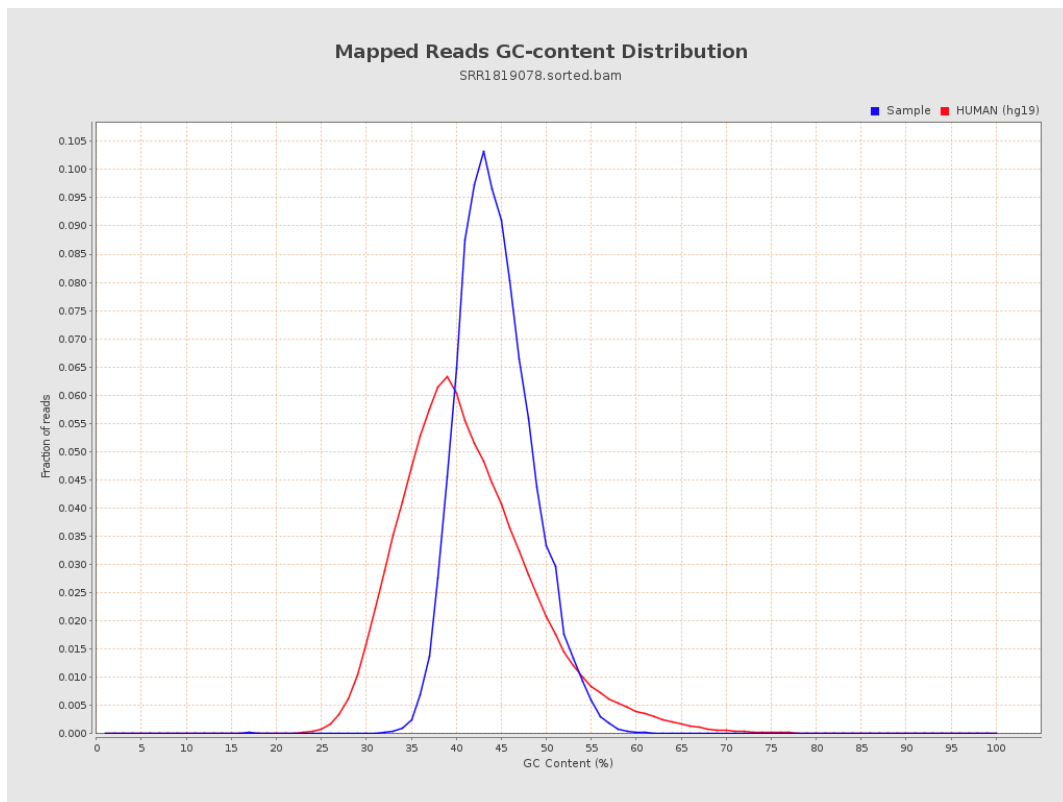
7. Results : Duplication Rate Histogram



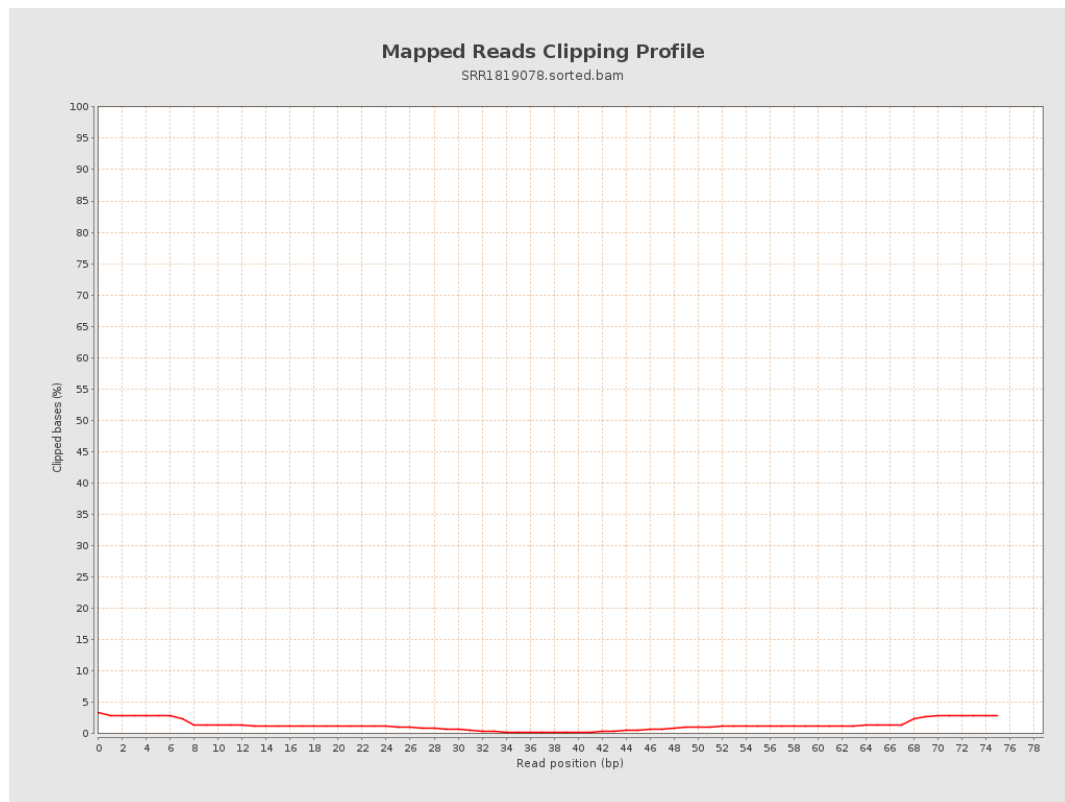
8. Results : Mapped Reads Nucleotide Content



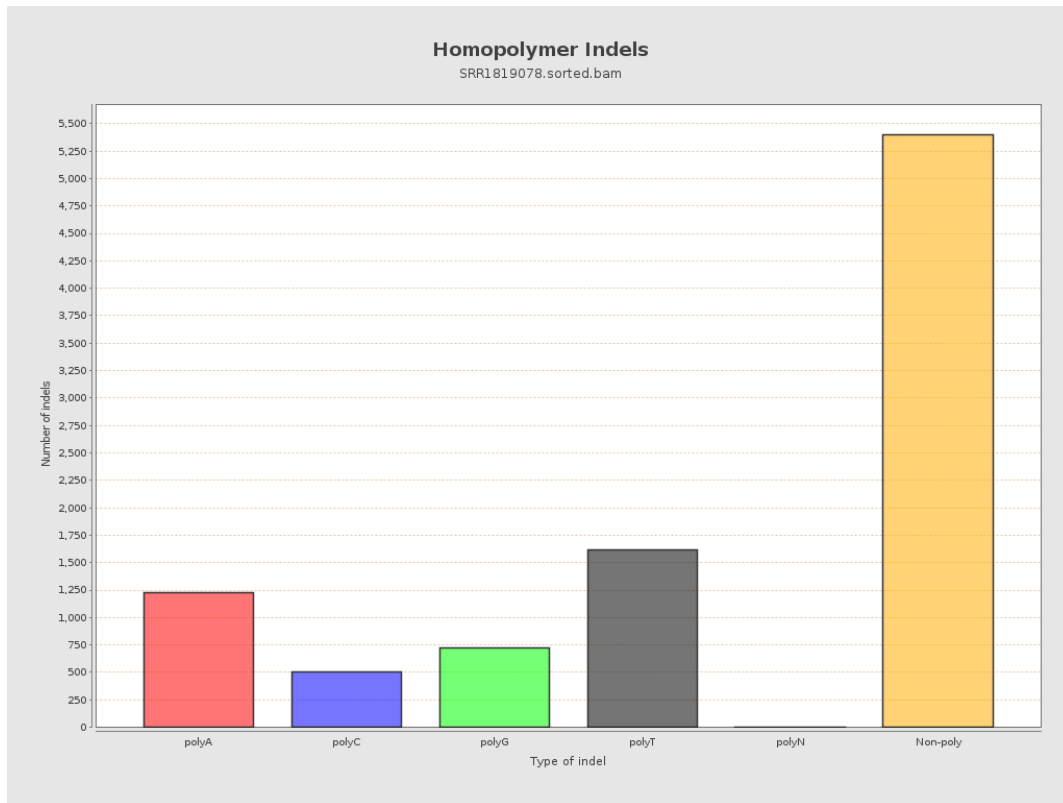
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

